Sequence Listing

(1) GENERAL INFORMATION:

   (i) APPLICANT: Garrard, Lisa J.
                Henner, Dennis J.
                Bass, Steven
                Greene, Ronald
                Lowman, Henry B.
                Wells, James A.
                Matthews, David J.

  (ii) TITLE OF INVENTION: ENRICHMENT METHOD FOR VARIANT PROTEINS WITH
                     ALTERED BINDING PROPERTIES

 (iii) NUMBER OF SEQUENCES: 43

  (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: Genentech, Inc.
      (B) STREET: 1 DNA Way
      (C) CITY: South San Francisco
      (D) STATE: California
      (E) COUNTRY: USA
      (F) ZIP: 94080

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: WinPatin (Genentech)

  (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER:
      (B) FILING DATE: 21-Nov-2000
      (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 08/922345
      (B) FILING DATE: 03-SEP-1997

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 08/463587
      (B) FILING DATE: 05-JUN-1995

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 08/050058
      (B) FILING DATE: 30-APR-1993

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: PCT/US91/09133
      (B) FILING DATE: 03-DEC-1991

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/743614
      (B) FILING DATE: 09-AUG-1991

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 07/715300
    (B) FILING DATE: 14-JUN-1991

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 07/683400
    (B) FILING DATE: 10-APR-1991

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 07/621667
    (B) FILING DATE: 03-DEC-1990

(viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME: Schwartz, Timothy R.
    (B) REGISTRATION NUMBER: 32171
    (C) REFERENCE/DOCKET NUMBER: P0645P4D2C3

(ix) TELECOMMUNICATION INFORMATION:
    (A) TELEPHONE: 650/225-7467
    (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCAGCTGTG GCTTCTAGAG TGGCGGCGGC TCTGGT 36

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGCTGTGGCT TCGGGCCCTT AGCATTTAAT GCGGTA 36

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCACAAACG AAGGGCCCCT AATTAAAGCC AGA 33

(2) INFORMATION FOR SEQ ID NO:4:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 30 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAATAATAAC GGGCTAGCCA AAAGAACTGG 30

(2) INFORMATION FOR SEQ ID NO:5:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 24 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CACGACAGAA TTCCCGACTG GAAA 24

(2) INFORMATION FOR SEQ ID NO:6:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 23 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGTTTCTAG AGTGAAATTG TTA 23

(2) INFORMATION FOR SEQ ID NO:7:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 21 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACATTCCTGG GTACCGTGCA G 21

(2) INFORMATION FOR SEQ ID NO:8:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 63 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTTCAGGAA GGACATGGAC NNSGTCNNSA CANNSCTGNN SATCGTGCAG 50

TGCCGCTCTG TGG 63

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGGTCTCCA CATACCTGAG GATC 24

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGGACAAGG TGTCGACATA CCTGCGCATC GTG 33

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCAGCTGTG GATTCTAGAG TGGCGGTGGC TCTGGT 36

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Gly Ser Cys Gly Phe Glu Ser Gly Gly Gly Ser Gly
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGACTGGGC AGATATTCAA GCAGACC 27

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCAAGAACT ACGGGTTACC CTGACTGCTT CAGGAAGG 38

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCATCGTGC AGTGCAGATC TGTGGAGGGC 30

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 66 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTACTCTAC TGCTTTCAGG AAGGACATGG ACNNSGTCNN SACANNSCTG 50

NNSATCGTGC AGTGCA 66

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCTGCACT GCACGATSNN CAGSNNTGTS NNGACSNNGT CCATGTCCTT 50

CCTGAAGCAG TAGA 64

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCTTTGACA GGTACCAGGA GTTTG 25

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAACTATAC CACTCTCGAG GTCTATTCGA TAA 33

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 66 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCGAGGCTCN NSGACAACGC GNNSCTGCGT GCTNNSCGTC TTNNSCAGCT 50

GGCCTTTGAC ACGTAC 66

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 base pairs

(B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGTCAAAGG CCAGCTGSNN AAGACGSNNA GCACGCAGSN NCGCGTTGTC 50

SNNGAGCC 58

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 65 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTTACTCTAC TGCTTCNNSA AGGACATGNN SAAGGTCAGC NNSTACCTGC 50

GCNNSGTGCA GTGCA 65

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCTGCACT GCACSNNGCG CAGGTASNNG CTGACCTTSN NCATGTCCTT 50

SNNGAAGCAG TAGA 64

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2178 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50

TGCTACAAAC GCGTACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100

TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG 150

GATGTGAATA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGCTCC 200

GAAACTACTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC 250

GCTTCTCTGG ATCCAGATCT GGGACGGATT TCACTCTGAC CATCAGCAGT 300

CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAGCAAC ATTATACTAC 350

TCCTCCCACG TTCGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG 400

CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450

GGAACTGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500

CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550

AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600

ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650

CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700

GGGGAGAGTG TTAAGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT 750

ACGCAAGTTC ACGTAAAAAG GGTATCTAGA GGTTGAGGTG ATTTTATGAA 800

AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA 850

CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG 900

CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCTG GCTTCAACAT 950

TAAAGACACC TATATACACT GGGTGCGTCA GGCCCCGGGT AAGGGCCTGG 1000

AATGGGTTGC AAGGATTTAT CCTACGAATG GTTATACTAG ATATGCCGAT 1050

AGCGTCAAGG GCCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC 1100

CTACCTGCAG ATGAACAGCC TGCGTGCTGA GGACACTGCC GTCTATTATT 1150

GTTCTAGATG GGGAGGGGAC GGCTTCTATG CTATGGACTA CTGGGGTCAA 1200

GGAACCCTGG TCACCGTCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT 1250

CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG 1300

GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC 1350

TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC 1400

CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACTGTGCCC TCTAGCAGCT 1450

TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC 1500

AAGGTGGACA AGAAAGTTGA GCCCAAATCT TGTGACAAAA CTCACACAGG 1550

GCCCTTCGTT TGTGAATATC AAGGCCAATC GTCTGACCTG CCTCAACCTC 1600

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CTGTCAATGC TGGCGGCGGC TCTGGTGGTG GTTCTGGTGG CGGCTCTGAG 1650

GGTGGTGGCT CTGAGGGTGG CGGTTCTGAG GGTGGCGGCT CTGAGGGAGG 1700

CGGTTCCGGT GGTGGCTCTG GTTCCGGTGA TTTTGATTAT GAAAAGATGG 1750

CAAACGCTAA TAAGGGGGCT ATGACCGAAA ATGCCGATGA AAACGCGCTA 1800

CAGTCTGACG CTAAAGGCAA ACTTGATTCT GTCGCTACTG ATTACGGTGC 1850

TGCTATCGAT GGTTTCATTG GTGACGTTTC CGGCCTTGCT AATGGTAATG 1900

GTGCTACTGG TGATTTTGCT GGCTCTAATT CCCAAATGGC TCAAGTCGGT 1950

GACGGTGATA ATTCACCTTT AATGAATAAT TTCCGTCAAT ATTTACCTTC 2000

CCTCCCTCAA TCGGTTGAAT GTCGCCCTTT TGTCTTTAGC GCTGGTAAAC 2050

CATATGAATT TTCTATTGAT TGTGACAAAA TAAACTTATT CCGTGGTGTC 2100

TTTGCGTTTC TTTTATATGT TGCCACCTTT ATGTATGTAT TTTCTACGTT 2150

TGCTAACATA CTGCGTAATA AGGAGTCT 2178

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 237 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1               5               10                      15

Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
                20              25                      30

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                35              40                      45

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln
                50              55                      60

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser
                65              70                      75

Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser
                80              85                      90

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                95              100                     105

Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
                110             115                     120
```

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```
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
              125             130             135

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
              140             145             150

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
              155             160             165

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
              170             175             180

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
              185             190             195

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
              200             205             210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
              215             220             225

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
              230             235
```

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 461 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
  1           5             10                      15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
              20             25                      30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
              35             40                      45

Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val
              50             55                      60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr
              65             70                      75

Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg
              80             85                      90

Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln
              95             100                     105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser
              110             115                     120
```

```
Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
             125             130             135

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
             140             145             150

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
             155             160             165

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
             170             175             180

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
             185             190             195

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
             200             205             210

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
             215             220             225

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
             230             235             240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Gly Pro Phe Val
             245             250             255

Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val
             260             265             270

Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
             275             280             285

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
             290             295             300

Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr
             305             310             315

Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala
             320             325             330

Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser
             335             340             345

Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp
             350             355             360

Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala
             365             370             . 375

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser
             380             385             390

Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
             395             400             405
```

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```
Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr
                410             415                     420

Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val
                425             430                     435

Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser
                440             445                     450

Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
                455             460
```

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTCGGGCCCT TCGCTGCTCA CTATACGCGT CAGTCGACTG ACCTGCCT 48

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCTGTGGCT TCGGGCCCGC CGCCGCGTCG ACTGGCGGTG GCTCT 45

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGCTGTGGCT TCGGGCCCGC CCCCGCGTCG ACTGGCGGTG GCTCT 45

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTCGCTGCT NNSNNSACCC GGCAA 25

(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCGATTGCCG GGTSNNSNNA GCAGCGAAGG GCC 33

(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCTCACT ACACCCGGCA A 21

(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCTGCTCACA TGACCCGGCA A 21

(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGCTCTCC ACACCCGGCA A 21

(2) INFORMATION FOR SEQ ID NO:35:

(i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 21 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

    GCTGCTCTGC ACACCCGGCA A 21

    (2) INFORMATION FOR SEQ ID NO:36:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 18 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

    GCTGCTCACA CCCGGCAA 18

    (2) INFORMATION FOR SEQ ID NO:37:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 21 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

    GCTGCTNNNC ACACCCGGCA A 21

    (2) INFORMATION FOR SEQ ID NO:38:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 21 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

    GCTGCTCACT ATACGCGTCA G 21

    (2) INFORMATION FOR SEQ ID NO:39:

        (i)   SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 21 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCTGCTCAGC ACACCCGGCA A 21

(2) INFORMATION FOR SEQ ID NO:40:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCTGCTACGC ACACCCGGCA A 21

(2) INFORMATION FOR SEQ ID NO:41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCTGCTCACT CCCGGCAA 18

(2) INFORMATION FOR SEQ ID NO:42:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCTGCTCATC ATACCCGGCA A 21

(2) INFORMATION FOR SEQ ID NO:43:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GCTGCTCACT TCCGGCAA 18